AMENDMENTS TO THE SPECIFICATION

At page 13, please delete the last paragraph, which spans pages 13 and 14, and insert the following replacement paragraph:

Using (B10.A.times.A).times.A backcross mice in which Rfv-3-associated phenotypes defined by titres of virus-neutralizing antibodies at post-infection day (PID) 15 were segregated, the present inventors performed detailed linkage analyses, and mapped this gene within a 3-Mbp segment of mouse chromosome 15 between D15Mit1 and D15Mit118 (FIGS. 2, 4, 5, 8). For physical mapping of the mouse markers, information found in the Ensemble Genome Browser ~~(http://www.ensembl.org)~~ on the segment of human chromosome 22 that is syntenic to this region of mouse chromosome 15 was utilized, and genes homologous between the two species were lined up with known simple sequence length polymorphism (SSLP) markers. As a result, several SSLP loci that are both polymorphic and located in the vicinity of the human homologues of Rfv-3-linked genes were identified (FIGS. 2, 4, 5, 8). Peripheral blood mononuclear cells (PBMCs) were provided by the previously documented ESN and HIV-infected individuals under written informed consent. All the ESNs enrolled were tested for serum HIV-1-reactive IgG, plasma HIV RNA, and HIV cDNA in cells of seminal or vaginal secretions, and none of them showed the presence of HIV-1, while the HIV-infected individuals were all positive in these tests. Using genomic DNA isolated from the above PBMCs as templates, alleles at the SSLP loci within chromosome 22 were identified by determining the sizes of PCR-amplified fragments (FIG. 3 and Table 1). As a result, the distribution of allele frequencies at the D22S277 locus was significantly different (X.sup.2=20.2 for the 2.times.11 table, p=0.020 by Fisher's exact test) between the ESN and HIV-infected groups. Viewed differently, ten of the 18 ESNs tested possessed at least one of the three distinct alleles at the D22S277 locus yielding a 154-, 156-, or 158-bp fragment, while one of these alleles were found in only two individuals among the 18 HIV-infected persons tested (X.sup.2=8.0, p=0.012 by Fisher's exact test). These three alleles are among the rare ones with reported frequencies of 7, 5, and 9%, respectively, in The Genome Database ~~(htt)://tadbwww.qdb.orog/)~~. On the other hand, the alleles yielding a 160- or 162-bp fragment are rather common among Caucasians with reported frequencies of 29 and 14%, respectively, and these latter alleles were observed at comparable frequencies in both groups (Table 1). Therefore, it should be emphasized that two of the 18 ESNs were homozygous for the allele yielding a 158-bp fragment, and three were zygotes between two of the above three rare alleles. In contrast, such zygotes of the rare alleles were not found among the HIV-infected individuals (5 of 18 vs 0 of 18 yielding p=0.045 by Fisher's exact test).

At page 23, please delete the last paragraph, whish spans pages 23 and 24, and insert the following replacement paragraph:

Genomic DNA was prepared from the tail tip of each mouse using DNeasy Tissue Kit (QIAGEN GmbH, Hilden, Germany) according to the manufacturer's instructions. A pair of oligonucleotide primers for each microsatellite locus was prepared based on the sequence information listed in a database within the Genetic and Physical Maps of the Mouse Genome site (~~http://www-genome.wi.mit.edu/cgi-bin/mouse/, The Whitehead Institute/MIT Center for Genome Research, Massachusetts~~), and were used for amplification by polymerase chain reaction (PCR) of genomic DNA fragments. 50 ng of each template DNA was subjected to 35 cycles of amplification with Quick Thermo Personal PCR Systems (Nippon Genetics, Tokyo, Japan), using a recombinant Taq polymerase (Invitrogen Life Technologies, Carlsbad, Calif.) according to the manufacturer's instructions. PCR products were separated by electrophoresis in 4% agarose gel and were visualized under a UV light by ethidium bromide staining.